

SEQUENCE LISTING

<110> Thompson, M. Craig
Long, Fan
Wobbe, C. Richard

<120> A NOVEL FUNGAL MULTISUBUNIT PROTEIN
COMPLEX CRITICAL FOR EXPRESSION OF FUNGAL PROTEINS

<130> 0342/1D516US2

<140> TBA

<141> Concurrently Herewith

<150> PCT/US99/02940

<151> 1999-02-08

<150> 60/074,100

<151> 1998-02-09

<160> 32

<170> FastSEQ for Windows Version 3.0

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<211> 4116

<212> DNA

<213> C. albicans

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Ile	Asp	Ala	Lys	Leu	Lys	Glu	Ser	Lys	His	Ala	Glu	Leu	Asn	Met	Asn	
385					390					395					400	
Asp	Glu	Lys	Leu	Leu	Leu	Met	Ile	Glu	Lys	Thr	Asn	Asn	Leu	Ala	Gln	
				405					410					415		
Gln	Lys	Gln	Gln	Leu	Asp	Ser	Ser	Asn	Leu	Ile	Leu	Pro	Leu	Asn	Glu	
			420					425					430			

Thr	Ile	Leu	Gln	Gln	Lys	Phe	Asn	Leu	Ser	Asn	Asp	Asp	Lys	Tyr	Gln
		435					440					445			
Ile	Leu	Lys	Lys	Thr	His	Gln	Thr	Lys	Val	Arg	Ser	Thr	Ile	Ser	Asn
	450					455					460				
Leu	Asn	Ile	Gln	His	Ser	Gln	Pro	Ala	Ile	Asn	Leu	Gln	Ser	Pro	Phe
465					470					475					480
Tyr	Lys	Val	Ala	Val	Pro	Arg	Tyr	Gln	Leu	Arg	His	Phe	His	Arg	Glu
				485					490					495	
Asn	Phe	Gly	Ser	His	Ile	Arg	Pro	Gly	Thr	Lys	Ile	Val	Phe	Ser	Lys
			500					505					510		
Leu	Lys	Ala	Arg	Lys	Arg	Lys	Arg	Asp	Lys	Gly	Lys	Asp	Val	Lys	Glu
		515					520					525			
Ser	Phe	Ser	Thr	Ser	Gln	Asp	Leu	Thr	Ile	Gly	Asp	Thr	Ala	Pro	Val
	530					535					540				
Tyr	Leu	Met	Glu	Tyr	Ser	Glu	Gln	Thr	Pro	Val	Ala	Leu	Ser	Lys	Phe
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Gly	Met	Ala	Asn	Lys	Leu	Ile	Asn	Tyr	Tyr	Arg	Lys	Ala	Asn	Glu	Gln
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Asp	Thr	Leu	Arg	Pro	Lys	Leu	Pro	Val	Gly	Glu	Thr	His	Val	Leu	Gly
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Val	Gln	Asp	Lys	Ser	Pro	Phe	Trp	Asn	Phe	Gly	Phe	Val	Glu	Pro	Gly
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His	Ile	Val	Pro	Thr	Leu	Tyr	Asn	Asn	Met	Ile	Arg	Ala	Pro	Val	Phe
	610					615					620				
Lys	His	Asp	Ile	Ser	Gly	Thr	Asp	Phe	Leu	Leu	Thr	Lys	Ser	Ser	Gly
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Phe	Gly	Ile	Ser	Asn	Arg	Phe	Tyr	Leu	Arg	Asn	Ile	Asn	His	Leu	Phe
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Thr	Val	Gly	Gln	Thr	Phe	Pro	Val	Glu	Glu	Ile	Pro	Gly	Pro	Asn	Ser
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Arg	Lys	Val	Thr	Ser	Met	Lys	Ala	Thr	Arg	Leu	Lys	Met	Ile	Ile	Tyr
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Lys	Glu	Phe	Met	Lys	Tyr	Gln	Arg	Asp	Gly	Pro	Glu	Lys	Gly	Leu	Trp
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Arg	Leu	Lys	Asp	Asp	Glu	Lys	Leu	Leu	Asp	Asn	Glu	Ala	Val	Lys	Ser
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Leu	Ile	Thr	Pro	Glu	Gln	Ile	Ser	Gln	Val	Glu	Ser	Met	Ser	Gln	Gly
		755					760					765			
Leu	Gln	Phe	Gln	Glu	Asp	Asn	Glu	Ala	Tyr	Asn	Phe	Asp	Ser	Lys	Leu
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Lys	Ser	Leu	Glu	Glu	Asn	Leu	Leu	Pro	Trp	Asn	Ile	Thr	Lys	Asn	Phe
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Ile	Asn	Ser	Thr	Gln	Met	Arg	Ala	Met	Ile	Gln	Ile	His	Gly	Val	Gly
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Asp	Pro	Thr	Gly	Cys	Gly	Glu	Gly	Phe	Ser	Phe	Leu	Lys	Thr	Ser	Met
			820					825					830		
Lys	Gly	Gly	Phe	Val	Lys	Ser	Gly	Ser	Pro	Ser	Ser	Asn	Asn	Asn	Ser
		835					840					845			

Ser	Asn	Lys	Lys	Gly	Thr	Asn	Thr	His	Ser	Tyr	Asn	Val	Ala	Gln	Gln
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Gln	Lys	Ala	Tyr	Asp	Glu	Glu	Ile	Ala	Lys	Thr	Trp	Tyr	Thr	His	Thr
865					870					875					880
Lys	Ser	Leu	Ser	Ile	Ser	Asn	Pro	Phe	Glu	Glu	Met	Thr	Asn	Pro	Asp
				885					890						895
Glu	Ile	Asn	Gln	Thr	Asn	Lys	His	Val	Lys	Thr	Asp	Arg	Asp	Asp	Lys
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Lys	Ile	Leu	Lys	Ile	Val	Arg	Lys	Lys	Arg	Asp	Glu	Asn	Gly	Ile	Ile
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Gln	Arg	Gln	Thr	Ile	Phe	Ile	Arg	Asp	Pro	Arg	Val	Ile	Gln	Gly	Tyr
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Ile	Lys	Ile	Lys	Glu	Gln	Asp	Lys	Glu	Asp	Val	Asn	Lys	Leu	Leu	Glu
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Glu	Asp	Thr	Ser	Lys	Ile	Asn	Asn	Leu	Glu	Glu	Leu	Glu	Lys	Gln	Lys
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Lys	Leu	Leu	Gln	Leu	Glu	Leu	Ala	Asn	Leu	Glu	Lys	Ser	Gln	Gln	Arg
			980					985					990		
Arg	Ala	Ala	Arg	Gln	Asn	Ser	Lys	Arg	Asn	Gly	Gly	Ala	Thr	Arg	Thr
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Lys	Ala	Ala	Arg	Asn	Lys	Gly	Lys	Asn	Thr	Thr	Arg	Arg	Cys	Ala	Thr
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Cys	Gly	Gln	Ile	Gly	His	Ile	Arg	Thr	Asn	Lys	Ser	Cys	Pro	Met	Tyr
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 <212> PRT
 <213> S. pombe

<400> 4

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Asp	Met	Ser	Val	Ile	Asn	Ser	Leu	Leu	Gly	Asp	Thr	Asn	Asn	Pro	Gly
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Met	Asn	Glu	Ser	Pro	Lys	Ile	Leu	Asp	Ser	Ser	Phe	Glu	Asn	Ser	Asn
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Pro	Gln	Asp	Gly	Pro	Asn	Tyr	Glu	Asp	Phe	Asp	Phe	Met	Gly	Ser	Ile
65					70					75					80
His	Lys	Glu	Phe	Gly	Asn	Asn	Ile	Asn	Glu	Met	Asp	Asp	Met	Glu	Asp
				85					90					95	
Val	Ser	Asp	Asp	Asn	Leu	Pro	Glu	Glu	Glu	Gln	Ala	Val	Asn	Tyr	Thr
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Gly	Asp	Lys	Asp	Asp	Glu	Asp	Phe	Gly	Lys	Leu	Leu	Ala	Lys	Glu	Met
		115					120					125			
Gly	Glu	Glu	Ala	Ala	Gly	Gln	Val	Leu	Ser	Gly	Val	Gly	Phe	Ser	Ile

130	Pro	Ser	Gly	Leu	Val	135	Pro	Pro	Ser	Glu	Pro	Ser	140	Lys	Thr	Val	Ser	Ser
145	Thr	Thr	Glu	Glu	Leu	150	Gln	Asn	Glu	Ala	Gln	Ile	155	Arg	Glu	Ser	Ile	Val
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	Lys	Thr	Phe	Phe	Pro	180	Thr	Phe	Glu	Arg	Gly	Val	185	Leu	Leu	Asn	Phe	Ser
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	Asp	Tyr	Ala	Ile	Ile	230	Phe	Asn	Ser	Lys	Lys	Ser	235	Leu	Pro	Leu	Lys	Arg
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	Asn	Val	Val	Ser	Pro	245	Ile	Ser	Thr	His	Thr	Lys	250	Lys	Arg	Arg	Arg	Thr
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	Ala	Asn	Thr	Ser	Gln	260	Arg	Asn	Asp	Gly	Leu	Asp	265	Leu	Asn	Thr	Val	Phe
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	Gln	Arg	Asn	Ser	Leu	355	Ala	Trp	Lys	Phe	Asn	Ile	360	Ser	Asn	Asp	Pro	Ala
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	Ser	Gln	Leu	Ala	Ile	385	Glu	His	Ala	Ala	Phe	Ala	390	Glu	Lys	Leu	Thr	Phe
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	Pro	Tyr	Tyr	Lys	Thr	405	Arg	Leu	Ser	Lys	Arg	Ala	410	Val	Arg	Ser	Tyr	His
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	Leu	Ile	Val	Arg	Lys	435	Arg	Ser	Lys	Asp	Lys	His	440	Lys	Ser	Glu	Arg	Glu
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	Leu	Ile	Pro	Thr	Thr	450	Lys	Glu	Ile	Thr	Met	Gly	455	Asp	Thr	Thr	His	Ala
					455								460					
	Ile	Leu	Val	Glu	Phe	465	Ser	Glu	Glu	His	Pro	Ala	470	Val	Leu	Ser	Asn	Ala
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	Gly	Met	Ala	Ser	Arg	485	Ile	Val	Asn	Tyr	Tyr	Arg	490	Lys	Lys	Asn	Glu	Gln
					490								495					
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					505								510					
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	Glu	Ile	Thr	Pro	Thr	530	Leu	Tyr	Asn	Lys	Met	Ile	535	Arg	Ala	Pro	Leu	Phe
					535								540					
	Lys	His	Glu	Val	Pro	545	Pro	Thr	Asp	Phe	Ile	Leu	550	Ile	Arg	Asn	Ser	Ser

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					565						570							575	
	Ser	Gly	Gln	Thr	Phe	Pro	Val	Thr	Asp	Val	Pro	Gly	Pro	His	Ser	Arg			
				580					585							590			
	Lys	Val	Thr	Thr	Ala	Ser	Lys	Asn	Arg	Leu	Lys	Met	Leu	Val	Phe	Arg			
			595					600					605						
	Leu	Ile	Arg	Arg	Ser	Pro	Asn	Gly	Gly	Leu	Phe	Ile	Arg	Gln	Leu	Ser			
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	Leu	Lys	Ser	Asn	Glu	Val	Val	Pro	Asp	Glu	Ala	Gly	Thr	Arg	Ser	Met			
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	Val	Ser	Pro	Glu	Thr	Val	Cys	Leu	Leu	Glu	Ser	Met	Gln	Val	Gly	Val			
			675					680					685						
	Arg	Gln	Leu	Glu	Asp	Ala	Gly	Tyr	Gly	Lys	Thr	Met	Asp	Glu	Ile	Asn			
		690					695					700							
	Asp	Asp	Glu	Asp	Glu	Glu	Gln	Pro	Ala	Glu	Gln	Leu	Leu	Ala	Pro	Trp			
	705				710						715								
	Ile	Thr	Thr	Arg	Asn	Phe	Ile	Asn	Ala	Thr	Gln	Gly	Lys	Ala	Met	Leu			
				725						730					735				
	Thr	Leu	Phe	Gly	Glu	Gly	Asp	Pro	Thr	Gly	Ile	Gly	Glu	Gly	Tyr	Ser			
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	Phe	Ile	Arg	Thr	Ser	Met	Lys	Gly	Gly	Phe	Lys	Pro	Ala	Gly	Glu	Thr			
			755					760					765						
	Ala	Asp	Asp	Lys	Pro	Glu	Pro	Gln	Thr	Lys	Asn	Ala	His	Ala	Tyr	Asn			
		770					775					780							
	Val	Ala	Lys	Gln	Gln	Arg	Ala	Tyr	Glu	Glu	Glu	Ile	Asn	Arg	Ile	Trp			
	785				790						795								
	Asn	Ala	Gln	Lys	Arg	Gly	Leu	Ser	Ile	Asn	Asn	Leu	Glu	Glu	Leu	Ala			
				805						810					815				
	Lys	Lys	Tyr	Gly	Ile	Asn	Ser	Ile	His	Asp	Asp	Tyr	Val	Glu	Ser	Asn			
			820						825					830					
	Glu	Glu	Thr	Thr	Arg	Glu	Glu	Thr	Pro	Ser	Ser	Asp	Lys	Val	Leu	Arg			
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	Ile	Val	Arg	Leu	Tyr	Arg	Asp	Lys	Asn	Gly	Asn	Leu	Glu	Arg	Lys	Gln			
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	Arg	Glu	Ile	Asp	Glu	Gln	Ser	Thr	Ala	Leu	Asp	Ala	Val	Val	Pro	Thr			
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	Gly	Asp	Glu	Ala	Ile	Asp	Arg	Arg	Asn	Arg	Arg	Arg	Leu	Glu	Gln	Glu			
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	Leu	Ala	Lys	Ser	Gln	Lys	Asn	Trp	Glu	Arg	Arg	Arg	Ala	Arg	His	Ala			
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		930					935					940							
	Arg	Lys	Cys	Ser	Asn	Cys	Gly	Gln	Val	Gly	His	Met	Lys	Thr	Asn	Lys			
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Asp Lys Asn

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<400> 5

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Met	Leu	Leu	Glu	Val	Ile	Asp	Leu	Lys	Glu	Ala	Glu	Pro	Pro	Ser	Asp
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Asp	Glu	Glu	Glu	Glu	Asp	Ala	Arg	Pro	Ser	Ala	Val	Ser	Ala	Ser	Gly
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Gly	Met	Ser	Ala	Phe	Asp	Ala	Leu	Lys	Ala	Gly	Val	Lys	Arg	Glu	Glu
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Arg	Glu	Asp	Gly	Ala	Val	Lys	Ala	Gln	Asp	Asp	Ala	Ile	Asp	Tyr	Ser
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Asp	Ile	Thr	Glu	Leu	Ser	Glu	Asp	Cys	Pro	Arg	Thr	Pro	Pro	Glu	Glu
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Thr	Ser	Thr	Tyr	Asp	Asp	Leu	Glu	Asp	Ala	Ile	Pro	Ala	Ser	Lys	Val
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Glu	Ala	Lys	Leu	Thr	Lys	Asp	Asp	Lys	Glu	Leu	Met	Pro	Pro	Pro	Ser
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Ala	Pro	Met	Arg	Ser	Gly	Ser	Gly	Gly	Gly	Ile	Glu	Glu	Pro	Ala	Lys
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Ser	Asn	Asp	Ala	Ser	Ser	Pro	Ser	Asp	Asp	Ser	Lys	Ser	Thr	Asp	Ser
	195						200					205			
Lys	Asp	Ala	Asp	Arg	Lys	Leu	Asp	Thr	Pro	Leu	Ala	Asp	Ile	Leu	Pro
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Ser	Lys	Tyr	Gln	Asn	Val	Asp	Val	Arg	Glu	Leu	Phe	Pro	Asp	Phe	Arg
225					230					235					240
Pro	Gln	Lys	Val	Leu	Arg	Phe	Ser	Arg	Leu	Phe	Gly	Pro	Gly	Lys	Pro
				245					250					255	
Thr	Ser	Leu	Pro	Gln	Ile	Trp	Arg	His	Val	Arg	Lys	Arg	Arg	Arg	Lys
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Tyr	Ala	Ala	Glu	Pro	Thr	Pro	Ala	Glu	Cys	Met	Ser	Asp	Asp	Glu	Asp
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Lys	Leu	Leu	Gly	Asp	Phe	Asn	Ser	Glu	Asp	Val	Arg	Pro	Glu	Gly	Pro
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Gln	Leu	His	Trp	Glu	Asp	Asp	Val	Val	Trp	Asp	Gly	Asn	Asp	Ile	Lys	
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Ala	Lys	Val	Leu	Gln	Lys	Leu	Asn	Ser	Lys	Thr	Asn	Ala	Ala	Gly	Trp	
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Lys	Pro	Ser	Met	Pro	Val	Gly	Ser	Gly	Ser	Ser	Lys	Gln	Gly	Ser	Gly	
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Leu	Ile	Tyr	Tyr	Lys	Trp	Glu	Asp	Glu	Val	Ile	Trp	Asp	Ala	Gln	Gln	
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Val	Ser	Lys	Val	Pro	Lys	Pro	Lys	Val	Leu	Thr	Leu	Asp	Pro	Asn	Asp	
	530					535					540					
Glu	Asn	Ile	Ile	Leu	Gly	Ile	Pro	Asp	Asp	Ile	Asp	Pro	Ser	Lys	Ile	
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Asn	Lys	Ser	Thr	Gly	Pro	Pro	Pro	Lys	Ile	Lys	Ile	Pro	His	Pro	His	
				565				570						575		
Val	Lys	Lys	Ser	Lys	Ile	Leu	Leu	Gly	Lys	Ala	Gly	Val	Ile	Asn	Val	
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Pro	Phe	Asn	Ile	Ser	Asn	Asp	Thr	Tyr	Tyr	Thr	Pro	Lys	Thr	Glu	Pro	
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Thr	Leu	Arg	Leu	Lys	Val	Gly	Gly	Asn	Leu	Ile	Gln	His	Ser	Thr	Pro	
625					630					635					640	
Val	Val	Glu	Leu	Arg	Ala	Pro	Phe	Val	Pro	Thr	His	Met	Gly	Pro	Met	
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Asn	Val	Arg	Ala	Phe	His	Arg	Pro	Pro	Leu	Lys	Lys	Tyr	Ser	His	Gly	
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Pro	Met	Ala	Gln	Ser	Ile	Pro	His	Pro	Val	Phe	Pro	Leu	Leu	Lys	Thr	
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Ile	Ala	Lys	Lys	Ala	Lys	Gln	Arg	Glu	Val	Glu	Arg	Ile	Ala	Ser	Gly	
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Gly	Gly	Asp	Val	Phe	Phe	Met	Arg	Asn	Pro	Glu	Asp	Leu	Ser	Gly	Arg	
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			740					745					750			

Lys	Ala	Glu	Lys	Asp	Ser	Gly	Pro	Gln	Asp	Tyr	Val	Tyr	Gly	Glu	Val
		755					760					765			
Ala	Phe	Ala	His	Thr	Ser	Pro	Phe	Leu	Gly	Ile	Leu	His	Pro	Gly	Gln
	770					775					780				
Cys	Ile	Gln	Ala	Ile	Glu	Asn	Asn	Met	Tyr	Arg	Ala	Pro	Ile	Tyr	Pro
785					790					795					800
His	Lys	Met	Ala	His	Asn	Asp	Phe	Leu	Val	Ile	Arg	Thr	Arg	Asn	Asn
				805					810					815	
Tyr	Trp	Ile	Arg	Ser	Val	Asn	Ser	Ile	Tyr	Thr	Val	Gly	Gln	Glu	Cys
			820					825					830		
Pro	Leu	Tyr	Glu	Val	Pro	Gly	Pro	Asn	Ser	Lys	Arg	Ala	Asn	Asn	Phe
		835					840					845			
Thr	Arg	Asp	Phe	Leu	Gln	Val	Phe	Ile	Tyr	Arg	Leu	Phe	Trp	Lys	Ser
	850					855					860				
Arg	Asp	Asn	Pro	Arg	Arg	Ile	Arg	Met	Asp	Asp	Ile	Lys	Gln	Ala	Phe
865					870					875					880
Pro	Ala	His	Ser	Glu	Ser	Ser	Ile	Arg	Lys	Arg	Leu	Lys	Gln	Cys	Ala
				885					890					895	
Asp	Phe	Lys	Arg	Thr	Gly	Met	Asp	Ser	Asn	Trp	Trp	Val	Ile	Lys	Pro
			900					905					910		
Glu	Phe	Arg	Leu	Pro	Ser	Glu	Glu	Glu	Ile	Arg	Ala	Met	Val	Ser	Pro
		915					920					925			
Glu	Gln	Cys	Cys	Ala	Tyr	Phe	Ser	Met	Ile	Ala	Ala	Glu	Gln	Arg	Leu
	930					935					940				
Lys	Asp	Ala	Gly	Tyr	Gly	Glu	Lys	Phe	Leu	Phe	Ala	Pro	Gln	Glu	Asp
945					950					955					960
Asp	Asp	Glu	Glu	Ala	Gln	Leu	Lys	Leu	Asp	Asp	Glu	Val	Lys	Val	Ala
				965					970					975	
Pro	Trp	Asn	Thr	Thr	Arg	Ala	Tyr	Ile	Gln	Ala	Met	Arg	Gly	Lys	Cys
			980					985					990		
Leu	Leu	Gln	Leu	Ser	Gly	Pro	Ala	Asp	Pro	Thr	Gly	Cys	Gly	Glu	Gly
		995				1000						1005			
Phe	Ser	Tyr	Val	Arg	Val	Pro	Asn	Lys	Pro	Thr	Gln	Thr	Lys	Glu	Glu
	1010					1015					1020				
Gln	Glu	Ser	Gln	Pro	Lys	Arg	Ser	Val	Thr	Gly	Thr	Asp	Ala	Asp	Leu
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Arg	Arg	Leu	Pro	Leu	Gln	Arg	Ala	Lys	Glu	Leu	Leu	Arg	Gln	Phe	Lys
				1045					1050					1055	
Val	Pro	Glu	Glu	Glu	Ile	Lys	Lys	Leu	Ser	Arg	Trp	Glu	Val	Ile	Asp
			1060					1065					1070		
Val	Val	Arg	Thr	Leu	Ser	Thr	Glu	Lys	Ala	Lys	Ala	Gly	Glu	Glu	Gly
		1075					1080					1085			
Met	Asp	Lys	Phe	Ser	Arg	Gly	Asn	Arg	Phe	Ser	Ile	Ala	Glu	His	Gln
	1090					1095					1100				
Glu	Arg	Tyr	Lys	Glu	Glu	Cys	Gln	Arg	Ile	Phe	Asp	Leu	Gln	Asn	Arg
1105					1110					1115					112
Val	Leu	Ala	Ser	Ser	Glu	Val	Leu	Ser	Thr	Asp	Glu	Ala	Glu	Ser	Ser
				1125					1130					1135	
Ala	Ser	Glu	Glu	Ser	Asp	Leu	Glu	Glu	Leu	Gly	Lys	Asn	Leu	Glu	Asn
			1140					1145					1150		
Met	Leu	Ser	Asn	Lys	Lys	Thr	Ser	Thr	Gln	Leu	Ser	Arg	Glu	Arg	Glu
			1155				1160						1165		

Glu	Leu	Glu	Arg	Gln	Glu	Leu	Leu	Arg	Gln	Leu	Asp	Glu	Glu	His	Gly	
1170					1175					1180						
Gly	Pro	Ser	Gly	Ser	Gly	Gly	Ala	Lys	Gly	Ala	Lys	Gly	Lys	Asp	Asp	
1185					1190					1195					120	
Pro	Gly	Gln	Gln	Met	Leu	Ala	Thr	Asn	Asn	Gln	Gly	Arg	Ile	Leu	Arg	
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Ile	Thr	Arg	Thr	Phe	Arg	Gly	Asn	Asp	Gly	Lys	Glu	Tyr	Thr	Arg	Val	
			1220					1225					1230			
Glu	Thr	Val	Arg	Arg	Gln	Pro	Val	Ile	Asp	Ala	Tyr	Ile	Lys	Ile	Arg	
		1235					1240					1245				
Thr	Thr	Lys	Asp	Glu	Gln	Phe	Ile	Lys	Gln	Phe	Ala	Thr	Leu	Asp	Glu	
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Gln	Gln	Lys	Glu	Glu	Met	Lys	Arg	Glu	Lys	Arg	Arg	Ile	Gln	Glu	Gln	
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Leu	Arg	Arg	Ile	Lys	Arg	Asn	Gln	Glu	Arg	Glu	Arg	Leu	Ala	Gln	Leu	
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Ala	Gln	Asn	Gln	Lys	Leu	Gln	Pro	Gly	Gly	Met	Pro	Thr	Ser	Leu	Gly	
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Asp	Pro	Lys	Ser	Ser	Gly	Gly	His	Ser	His	Lys	Glu	Arg	Asp	Ser	Gly	
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Tyr	Lys	Glu	Val	Ser	Pro	Ser	Arg	Lys	Lys	Phe	Lys	Leu	Lys	Pro	Asp	
1330						1335				1340						
Leu	Lys	Leu	Lys	Cys	Gly	Ala	Cys	Gly	Gln	Val	Gly	His	Met	Arg	Thr	
1345					1350					1355					136	
Asn	Lys	Ala	Cys	Pro	Leu	Tyr	Ser	Gly	Met	Gln	Ser	Ser	Leu	Ser	Gln	
				1365					1370					1375		
Ser	Asn	Pro	Ser	Leu	Ala	Asp	Asp	Phe	Asp	Glu	Gln	Ser	Glu	Lys	Glu	
			1380					1385					1390			
Met	Thr	Met	Asp	Asp	Asp	Asp	Leu	Val	Asn	Val	Asp	Gly	Thr	Lys	Val	
		1395					1400					1405				
Thr	Leu	Ser	Ser	Lys	Ile	Leu	Lys	Arg	His	Gly	Gly	Asp	Asp	Gly	Lys	
1410					1415							1420				
Arg	Arg	Ser	Gly	Ser	Ser	Gly	Phe	Thr	Leu	Lys	Val	Pro	Arg	Asp		
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Ala	Met	Gly	Lys	Lys	Lys	Arg	Arg	Val	Gly	Gly	Asp	Leu	His	Cys	Asp	
				1445					1450					1455		
Tyr	Leu	Gln	Arg	His	Asn	Lys	Thr	Ala	Asn	Arg	Arg	Arg	Thr	Asp	Pro	
			1460					1465					1470			
Val	Val	Val	Leu	Ser	Ser	Ile	Leu	Glu	Ile	Ile	His	Asn	Glu	Leu	Arg	
		1475					1480					1485				
Ser	Met	Pro	Asp	Val	Ser	Pro	Phe	Leu	Phe	Pro	Val	Ser	Ala	Lys	Lys	
1490						1495					1500					
Val	Pro	Asp	Tyr	Tyr	Arg	Val	Val	Thr	Lys	Pro	Met	Asp	Leu	Gln	Thr	
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Met	Arg	Glu	Tyr	Ile	Arg	Gln	Arg	Arg	Tyr	Thr	Ser	Arg	Glu	Met	Phe	
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Leu	Glu	Asp	Leu	Lys	Gln	Ile	Val	Asp	Asn	Ser	Leu	Ile	Tyr	Asn	Gly	
			1540					1545					1550			
Pro	Gln	Ser	Ala	Tyr	Thr	Leu	Ala	Ala	Gln	Arg	Met	Phe	Ser	Ser	Cys	
		1555					1560					1565				
Phe	Glu	Leu	Leu	Ala	Glu	Arg	Glu	Asp	Lys	Leu	Met	Arg	Leu	Glu	Lys	
1570						1575					1580					

Ala	Ile	Asn	Pro	Leu	Leu	Asp	Asp	Asp	Asp	Gln	Val	Ala	Leu	Ser	Phe	1585	1590	1595	160
Ile	Phe	Asp	Lys	Leu	His	Ser	Gln	Ile	Lys	Gln	Leu	Pro	Glu	Ser	Trp	1605	1610	1615	1615
Pro	Phe	Leu	Lys	Pro	Val	Asn	Lys	Lys	Gln	Val	Lys	Asp	Tyr	Tyr	Thr	1620	1625	1630	1630
Val	Ile	Lys	Arg	Pro	Met	Asp	Leu	Glu	Thr	Ile	Gly	Lys	Asn	Ile	Glu	1635	1640	1645	1645
Ala	His	Arg	Tyr	His	Ser	Arg	Ala	Glu	Tyr	Leu	Ala	Asp	Ile	Glu	Leu	1650	1655	1660	1660
Ile	Ala	Thr	Asn	Cys	Glu	Gln	Tyr	Asn	Gly	Ser	Asp	Thr	Arg	Tyr	Thr	1665	1670	1675	168
Lys	Phe	Ser	Lys	Lys	Ile	Leu	Glu	Tyr	Ala	Gln	Thr	Gln	Leu	Ile	Glu	1685	1690	1695	1695
Phe	Ser	Glu	His	Cys	Gly	Gln	Leu	Glu	Asn	Asn	Ile	Ala	Lys	Thr	Gln	1700	1705	1710	1710
Glu	Arg	Ala	Arg	Glu	Asn	Ala	Pro	Glu	Phe	Asp	Glu	Ala	Trp	Gly	Asn	1715	1720	1725	1725
Asp	Asp	Tyr	Asn	Phe	Asp	Arg	Gly	Ser	Arg	Ala	Ser	Ser	Pro	Gly	Asp	1730	1735	1740	1740
Asp	Tyr	Ile	Asp	Val	Glu	Gly	His	Gly	Gly	His	Ala	Ser	Ser	Ser	Asn	1745	1750	1755	176
Ser	Ile	His	Arg	Ser	Met	Gly	Ala	Glu	Ala	Gly	Ser	Ser	His	Thr	Ala	1765	1770	1775	1775
Pro	Ala	Val	Arg	Lys	Pro	Ala	Pro	Pro	Gly	Pro	Gly	Glu	Val	Lys	Arg	1780	1785	1790	1790
Gly	Arg	Gly	Arg	Pro	Arg	Lys	Gln	Arg	Asp	Pro	Val	Glu	Glu	Asp	Leu	1795	1800	1805	1805
Gln	Cys	Ser	Thr	Asp	Asp	Glu	Asp	Asp	Asp	Glu	Glu	Glu	Asp	Phe	Gln	1810	1815	1820	1820
Glu	Val	Ser	Glu	Asp	Glu	Asn	Asn	Ala	Ala	Ser	Ile	Leu	Asp	Gln	Gly	1825	1830	1835	184
Glu	Arg	Ile	Asn	Ala	Pro	Ala	Asp	Ala	Met	Asp	Gly	Met	Phe	Asp	Pro	1845	1850	1855	1855
Lys	Asn	Ile	Lys	Thr	Glu	Ile	Asp	Leu	Glu	Ala	His	Gln	Met	Ala	Asp	1860	1865	1870	1870
Glu	Ser	Met	Asp	Val	Asp	Pro	Asn	Tyr	Asp	Pro	Ser	Asp	Phe	Leu	Ala	1875	1880	1885	1885
Met	His	Lys	Gln	Arg	Gln	Ser	Leu	Gly	Glu	Pro	Ser	Ser	Leu	Gln	Gly	1890	1895	1900	1900
Ala	Phe	Thr	Asn	Phe	Leu	Ser	His	Glu	Gln	Asp	Asp	Asn	Gly	Pro	Tyr	1905	1910	1915	192
Asn	Pro	Ala	Glu	Ala	Ser	Thr	Ser	Ala	Ala	Ser	Gly	Ala	Asp	Leu	Gly	1925	1930	1935	1935
Met	Asp	Ala	Ser	Met	Ala	Met	Gln	Met	Ala	Pro	Glu	Met	Pro	Val	Asn	1940	1945	1950	1950
Thr	Met	Asn	Asn	Gly	Met	Gly	Ile	Asp	Asp	Asp	Leu	Asp	Ile	Ser	Glu	1955	1960	1965	1965
Ser	Asp	Glu	Glu	Asp	Asp	Gly	Ser	Arg	Val	Arg	Ile	Lys	Lys	Glu	Val	1970	1975	1980	1980
Phe	Asp	Asp	Gly	Asp	Tyr	Ala	Leu	Gln	His	Gln	Gln	Met	Gly	Gln	Ala	1985	1990	1995	200

Ala Ser Gln Ser Gln Ile Tyr Met Val Asp Ser Ser Asn Glu Pro Thr
 2005 2010 2015
 Thr Leu Asp Tyr Gln Gln Pro Pro Gln Leu Asp Phe Gln Gln Val Gln
 2020 2025 2030
 Glu Met Glu Gln Leu Gln His Gln Val Met Pro Pro Met Gln Ser Glu
 2035 2040 2045
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 2050 2055 2060
 Thr Phe
 2065

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 <212> PRT
 <213> Homo sapiens

<400> 6
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 Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
 35 40 45
 Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
 50 55 60
 His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
 65 70 75 80
 Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
 85 90 95
 Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
 100 105 110
 Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
 115 120 125
 Gly Ser Leu Gln Pro Leu Cys His Ser Asp Tyr Asp Glu Asp Asp Tyr
 130 135 140
 Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
 145 150 155 160
 Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
 165 170 175
 Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met
 180 185 190
 Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
 195 200 205
 Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
 210 215 220
 Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
 225 230 235 240
 Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
 245 250 255
 Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
 260 265 270
 Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln

		275					280					285				
Lys	Ser	Leu	Trp	Asn	Tyr	Asp	Tyr	Ala	Pro	Pro	Pro	Pro	Pro	Glu	Gln	
	290					295					300					
Cys	Leu	Ser	Asp	Asp	Glu	Ile	Thr	Met	Met	Ala	Pro	Val	Glu	Ser	Lys	
305					310					315					320	
Phe	Ser	Gln	Ser	Thr	Gly	Asp	Ile	Asp	Lys	Val	Thr	Asp	Thr	Lys	Pro	
				325					330					335		
Arg	Val	Ala	Glu	Trp	Arg	Tyr	Gly	Pro	Ala	Arg	Leu	Trp	Tyr	Asp	Met	
			340					345					350			
Leu	Gly	Val	Pro	Glu	Asp	Gly	Ser	Gly	Phe	Asp	Tyr	Gly	Phe	Lys	Leu	
		355					360					365				
Arg	Lys	Thr	Glu	His	Glu	Pro	Val	Ile	Lys	Ser	Arg	Met	Ile	Glu	Glu	
	370					375					380					
Phe	Arg	Lys	Leu	Glu	Glu	Asn	Asn	Gly	Thr	Asp	Leu	Leu	Ala	Asp	Glu	
385					390					395					400	
Asn	Phe	Leu	Met	Val	Thr	Gln	Leu	His	Trp	Glu	Asp	Asp	Ile	Ile	Trp	
				405					410					415		
Asp	Gly	Glu	Asp	Val	Lys	His	Lys	Gly	Thr	Lys	Pro	Gln	Arg	Ala	Ser	
		420						425					430			
Leu	Ala	Gly	Trp	Leu	Pro	Ser	Ser	Met	Thr	Arg	Asn	Ala	Met	Ala	Tyr	
		435					440					445				
Asn	Val	Gln	Gln	Gly	Phe	Ala	Ala	Thr	Leu	Asp	Asp	Asp	Lys	Pro	Trp	
	450					455					460					
Tyr	Ser	Ile	Phe	Pro	Ile	Asp	Asn	Glu	Asp	Leu	Val	Tyr	Gly	Arg	Trp	
465					470					475					480	
Glu	Asp	Asn	Ile	Ile	Trp	Asp	Ala	Gln	Ala	Met	Pro	Arg	Leu	Leu	Glu	
				485				490						495		
Pro	Pro	Val	Leu	Thr	Leu	Asp	Pro	Asn	Asp	Glu	Asn	Leu	Ile	Leu	Glu	
		500						505					510			
Ile	Pro	Asp	Glu	Lys	Glu	Glu	Ala	Thr	Ser	Asn	Ser	Pro	Ser	Lys	Glu	
		515					520					525				
Ser	Lys	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Ser	Arg	Ile	Leu	Leu	Gly	Lys	
	530					535					540					
Thr	Gly	Val	Ile	Lys	Glu	Glu	Pro	Gln	Gln	Asn	Met	Ser	Gln	Pro	Glu	
545					550					555					560	
Val	Lys	Asp	Pro	Trp	Asn	Leu	Ser	Asn	Asp	Glu	Tyr	Tyr	Tyr	Pro	Lys	
				565					570					575		
Gln	Gln	Gly	Leu	Arg	Gly	Thr	Phe	Gly	Gly	Asn	Ile	Ile	Gln	His	Ser	
			580					585					590			
Ile	Pro	Ala	Val	Glu	Leu	Arg	Gln	Pro	Phe	Phe	Pro	Thr	His	Met	Gly	
		595					600					605				
Pro	Ile	Lys	Leu	Arg	Gln	Phe	His	Arg	Pro	Pro	Leu	Lys	Lys	Tyr	Ser	
	610					615					620					
Phe	Gly	Ala	Leu	Ser	Gln	Pro	Gly	Pro	His	Ser	Val	Gln	Pro	Leu	Leu	
625					630					635					640	
Lys	His	Ile	Lys	Lys	Lys	Ala	Lys	Met	Arg	Glu	Gln	Glu	Arg	Gln	Ala	
				645					650					655		
Ser	Gly	Gly	Gly	Glu	Met	Phe	Phe	Met	Arg	Thr	Pro	Gln	Asp	Leu	Thr	
		660						665					670			
Gly	Lys	Asp	Gly	Asp	Leu	Ile	Leu	Ala	Glu	Tyr	Ser	Glu	Glu	Asn	Gly	
	675						680					685				
Pro	Leu	Met	Met	Gln	Val	Gly	Met	Ala	Thr	Lys	Ile	Lys	Asn	Tyr	Tyr	

690		695		700
Lys Arg Lys Pro Gly	Lys Asp Pro Gly Ala	Pro Asp Cys Lys Tyr Gly		
705	710	715		720
Glu Thr Val Tyr Cys	His Thr Ser Pro Phe	Leu Gly Ser Leu His Pro		
	725	730		735
Gly Gln Leu Leu Gln	Ala Phe Glu Asn Asn	Leu Phe Arg Ala Pro Ile		
	740	745		750
Tyr Leu His Lys Met	Pro Glu Thr Asp Phe	Leu Ile Ile Arg Thr Arg		
	755	760		765
Gln Gly Tyr Tyr Ile	Arg Glu Leu Val Asp	Ile Phe Val Val Gly Gln		
	770	775		780
Gln Cys Pro Leu Phe	Glu Val Pro Gly Pro	Asn Ser Lys Arg Ala Asn		
785	790	795		800
Thr His Ile Arg Asp	Phe Leu Gln Val Phe	Ile Tyr Arg Leu Phe Trp		
	805	810		815
Lys Ser Lys Asp Arg	Pro Arg Arg Ile Arg	Met Glu Asp Ile Lys Lys		
	820	825		830
Ala Phe Pro Ser His	Ser Glu Ser Ser Ile	Arg Lys Arg Leu Lys Leu		
	835	840		845
Cys Ala Asp Phe Lys	Arg Thr Gly Met Asp	Ser Asn Trp Trp Val Leu		
	850	855		860
Lys Ser Asp Phe Arg	Leu Pro Thr Glu Glu	Glu Ile Arg Ala Met Val		
865	870	875		880
Ser Pro Glu Gln Cys	Cys Ala Tyr Tyr Ser	Met Ile Ala Ala Glu Gln		
	885	890		895
Arg Leu Lys Asp Ala	Gly Tyr Gly Glu Lys	Ser Phe Phe Ala Pro Glu		
	900	905		910
Glu Glu Asn Glu Glu	Asp Phe Gln Met Lys	Ile Asp Asp Glu Val Arg		
	915	920		925
Thr Ala Pro Trp Asn	Thr Thr Arg Ala Phe	Ile Ala Ala Met Lys Gly		
	930	935		940
Lys Cys Leu Leu Glu	Val Thr Gly Val Ala	Asp Pro Thr Gly Cys Gly		
945	950	955		960
Glu Gly Phe Ser Tyr	Val Lys Ile Pro Asn	Lys Pro Thr Gln Gln Lys		
	965	970		975
Asp Asp Lys Glu Pro	Gln Pro Val Lys Thr	Val Thr Gly Thr Asp		
	980	985		990
Ala Asp Leu Arg Arg	Leu Ser Leu Lys Asn	Ala Lys Gln Leu Leu Arg		
	995	1000		1005
Lys Phe Gly Val Pro	Glu Glu Glu Ile Lys	Lys Leu Ser Arg Trp Glu		
	1010	1015		1020
Val Ile Asp Val Val	Arg Thr Met Ser Thr	Glu Gln Ala Arg Ser Gly		
1025	1030	1035		104
Glu Gly Pro Met Ser	Lys Phe Ala Arg Gly	Ser Arg Phe Ser Val Ala		
	1045	1050		1055
Glu His Gln Glu Arg	Tyr Lys Glu Glu Cys	Gln Arg Ile Phe Asp Leu		
	1060	1065		1070
Gln Asn Lys Val Leu	Ser Ser Thr Glu Val	Leu Ser Thr Asp Thr Asp		
	1075	1080		1085
Ser Ser Ser Ala Glu	Asp Ser Asp Phe Glu	Glu Met Gly Lys Asn Ile		
	1090	1095		1100
Glu Asn Met Leu Gln	Asn Lys Lys Thr Ser	Ser Gln Leu Ser Arg Glu		

1105		1110		1115		112
Arg Glu Glu Gln Glu	Arg Lys Glu Leu Gln	Arg Met Leu Leu Ala Ala				
	1125		1130		1135	
Gly Ser Ala Ala Ser	Gly Asn Asn His	Arg Asp Asp Asp Thr Ala Ser				
	1140		1145		1150	
Val Thr Ser Leu Asn Ser Ser	Ala Thr Gly Arg Cys Leu Lys Ile Tyr					
	1155		1160		1165	
Arg Thr Phe Arg Asp Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr						
	1170		1175		1180	
Val Arg Lys Pro Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr						
	1185		1190		1195	120
Lys Asp Glu Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His						
	1205		1210		1215	
Arg Glu Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg						
	1220		1225		1230	
Arg Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu						
	1235		1240		1245	
Lys Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys Cys						
	1250		1255		1260	
Gly Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe Cys Pro						
	1265		1270		1275	128
Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val Ala Met Thr						
	1285		1290		1295	
Glu Glu Gln Glu Glu Glu Leu Glu Lys Thr Val Ile His Asn Asp Asn						
	1300		1305		1310	
Glu Glu Leu Ile Lys Val Glu Gly Thr Lys Ile Val Leu Gly Lys Gln						
	1315		1320		1325	
Leu Ile Glu Ser Ala Asp Glu Val Arg Arg Lys Ser Leu Val Leu Lys						
	1330		1335		1340	
Phe Pro Lys Gln Gln Leu Pro Pro Lys Lys Lys Arg Arg Val Gly Thr						
	1345		1350		1355	136
Thr Val His Cys Asp Tyr Leu Asn Arg Pro His Lys Ser Ile His Arg						
	1365		1370		1375	
Arg Arg Thr Asp Pro Met Val Thr Leu Ser Ser Ile Leu Glu Ser Ile						
	1380		1385		1390	
Ile Asn Asp Met Arg Asp Leu Pro Asn Thr Tyr Pro Phe His Thr Pro						
	1395		1400		1405	
Val Asn Ala Lys Val Val Lys Asp Tyr Tyr Lys Ile Ile Thr Arg Pro						
	1410		1415		1420	
Met Asp Leu Gln Thr Leu Arg Glu Asn Val Arg Lys Arg Leu Tyr Pro						
	1425		1430		1435	144
Ser Arg Glu Glu Phe Arg Glu His Leu Glu Leu Ile Val Lys Asn Ser						
	1445		1450		1455	
Ala Thr Tyr Asn Gly Pro Lys His Ser Leu Thr Gln Ile Ser Gln Ser						
	1460		1465		1470	
Met Leu Asp Leu Cys Asp Glu Lys Leu Lys Glu Lys Glu Asp Lys Leu						
	1475		1480		1485	
Ala Arg Leu Glu Lys Ala Ile Asn Pro Leu Leu Asp Asp Asp Asp Gln						
	1490		1495		1500	
Val Ala Phe Ser Phe Ile Leu Asp Asn Ile Val Thr Gln Lys Met Met						
	1505		1510		1515	152
Ala Val Pro Asp Ser Trp Pro Phe His His Pro Val Asn Lys Lys Phe						

				1525					1530					1535					
Val	Pro	Asp	Tyr	Tyr	Lys	Val	Ile	Val	Asn	Pro	Met	Asp	Leu	Glu	Thr				
			1540						1545					1550					
Ile	Arg	Lys	Asn	Ile	Ser	Lys	His	Lys	Tyr	Gln	Ser	Arg	Glu	Ser	Phe				
		1555							1560					1565					
Leu	Asp	Asp	Val	Asn	Leu	Ile	Leu	Ala	Asn	Ser	Val	Lys	Tyr	Asn	Gly				
	1570						1575						1580						
Pro	Glu	Ser	Gln	Tyr	Thr	Lys	Thr	Ala	Gln	Glu	Ile	Val	Asn	Val	Cys				
1585						1590				1595					160				
Tyr	Gln	Thr	Leu	Thr	Glu	Tyr	Asp	Glu	His	Leu	Thr	Gln	Leu	Glu	Lys				
			1605						1610					1615					
Asp	Ile	Cys	Thr	Ala	Lys	Glu	Ala	Ala	Leu	Glu	Glu	Ala	Glu	Leu	Glu				
			1620					1625					1630						
Ser	Leu	Asp	Pro	Met	Thr	Pro	Gly	Pro	Tyr	Thr	Pro	Gln	Pro	Pro	Asp				
		1635					1640					1645							
Leu	Tyr	Asp	Thr	Asn	Thr	Ser	Leu	Ser	Met	Ser	Arg	Asp	Ala	Ser	Val				
	1650					1655					1660								
Phe	Gln	Asp	Glu	Ser	Asn	Met	Ser	Val	Leu	Asp	Ile	Pro	Ser	Ala	Thr				
1665					1670					1675					168				
Pro	Glu	Lys	Gln	Val	Thr	Gln	Glu	Gly	Glu	Asp	Gly	Asp	Gly	Asp	Leu				
			1685						1690					1695					
Ala	Asp	Glu	Glu	Glu	Gly	Thr	Val	Gln	Gln	Pro	Gln	Ala	Ser	Val	Leu				
			1700					1705				1710							
Tyr	Glu	Asp	Leu	Leu	Met	Ser	Glu	Gly	Glu	Asp	Asp	Glu	Glu	Asp	Ala				
	1715						1720					1725							
Gly	Ser	Asp	Glu	Glu	Gly	Asp	Asn	Pro	Phe	Ser	Ala	Ile	Gln	Leu	Ser				
	1730					1735					1740								
Glu	Ser	Gly	Ser	Asp	Ser	Asp	Val	Gly	Ser	Gly	Gly	Ile	Arg	Pro	Lys				
1745					1750					1755					176				
Gln	Pro	Arg	Met	Leu	Gln	Glu	Asn	Thr	Arg	Met	Asp	Met	Glu	Asn	Glu				
			1765						1770				1775						
Glu	Ser	Met	Met	Ser	Tyr	Glu	Gly	Asp	Gly	Gly	Glu	Ala	Ser	His	Gly				
		1780					1785					1790							
Leu	Glu	Asp	Ser	Asn	Ile	Ser	Tyr	Gly	Ser	Tyr	Glu	Glu	Pro	Asp	Pro				
	1795						1800					1805							
Lys	Ser	Asn	Thr	Gln	Asp	Thr	Ser	Phe	Ser	Ser	Ile	Gly	Gly	Tyr	Glu				
	1810					1815					1820								
Val	Ser	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Gln	Arg	Ser	Gly					
1825					1830					1835					184				
Pro	Ser	Val	Leu	Ser	Gln	Val	His	Leu	Ser	Glu	Asp	Glu	Glu	Asp	Ser				
			1845						1850				1855						
Glu	Asp	Phe	His	Ser	Ile	Ala	Gly	Asp	Ser	Asp	Leu	Asp	Ser	Asp	Glu				
		1860						1865				1870							

<210> 7
 <211> 429
 <212> PRT
 <213> C. albicans

<400> 7
 Glu Leu Leu Leu Asn Asn Pro Leu Asp Asn Ser Lys Gln Asn Arg Gln
 1 5 10 15

Lys	Ile	Glu	Asn	Asp	Asn	Thr	Thr	Asn	Asn	Tyr	Asn	Gln	Asn	Asn	Ser	
			20					25					30			
Asn	Val	Gln	Asp	Glu	Glu	Glu	Asp	Asp	Asp	Ile	Phe	Asn	Gly	Gln	Ile	
		35					40					45				
Asn	Leu	Asp	Lys	Leu	Lys	Leu	Asp	Met	Asn	Asp	Pro	Asn	Leu	Leu	Phe	
	50					55					60					
Val	Pro	Ser	Lys	Lys	Val	Asp	Ala	Thr	Lys	Ser	Val	Val	Pro	Ser	Thr	
65					70					75					80	
Asp	Lys	Leu	Leu	Glu	Leu	Lys	Phe	Asn	Ile	Ser	Asn	Asp	Gln	Glu	Tyr	
				85					90					95		
Glu	Leu	Leu	Arg	Lys	Asn	Tyr	Asn	Thr	Lys	Gln	Arg	Ser	Gln	Leu	Ser	
			100					105					110			
Asn	Leu	Asn	Ile	Glu	His	Ser	Val	Pro	Ala	Leu	Arg	Leu	Gln	Thr	Pro	
		115					120					125				
Tyr	Tyr	Lys	Val	Lys	Leu	Ser	Thr	Asp	Glu	Thr	Arg	Ser	Phe	His	Arg	
	130					135					140					
Pro	Val	Phe	Asn	Val	Arg	Pro	Gly	Thr	Leu	Val	Ser	Phe	Ser	Lys	Leu	
145					150					155					160	
Lys	Leu	Arg	Lys	Arg	Lys	Lys	Asp	Lys	Gly	Lys	Ser	Leu	Gln	Gln	Ile	
				165					170					175		
Phe	Ser	Lys	Thr	Ser	Asp	Leu	Thr	Val	Ala	Asp	Thr	Gly	Asn	Ile	Ile	
			180					185					190			
Ala	Leu	Glu	Tyr	Ser	Glu	Gln	Tyr	Pro	Pro	Ile	Leu	Ser	Asn	Phe	Gly	
		195					200					205				
Met	Gly	Ser	Lys	Leu	Ile	Asn	Tyr	Tyr	Arg	Lys	Glu	Arg	Pro	Asn	Asp	
	210					215					220					
Thr	Ser	Arg	Pro	Lys	Ala	Gln	Ile	Gly	Glu	Thr	His	Ile	Leu	Gly	Val	
225					230					235					240	
Glu	Asp	Arg	Ser	Pro	Phe	Trp	Asn	Phe	Gly	Glu	Val	Ala	Pro	Gly	Asp	
				245					250					255		
Phe	Val	Pro	Thr	Leu	Tyr	Asn	Asn	Met	Val	Arg	Ala	Pro	Ile	Phe	Lys	
			260					265				270				
His	Asp	Asn	Lys	Pro	Thr	Asp	Phe	Leu	Leu	Val	Lys	Ser	Gln	Gly	Ala	
		275					280					285				
Gly	Ser	His	Gln	Lys	Phe	Tyr	Leu	Arg	Gly	Ile	Asn	Phe	Asn	Phe	Ala	
	290					295					300					
Val	Gly	Asn	Thr	Phe	Pro	Val	Glu	Val	Pro	Ala	Pro	His	Ser	Arg	Lys	
305					310					315					320	
Val	Thr	Asn	Ile	Ser	Lys	Asn	Arg	Leu	Lys	Met	Val	Val	Phe	Arg	Val	
				325					330					335		
Met	Asn	Ser	Leu	Gly	Val	Pro	Arg	Ile	Ser	Val	Lys	Asp	Val	Ser	Lys	
			340					345					350			
His	Phe	Pro	Glu	His	Ser	Asp	Met	Gln	Asn	Arg	Gln	Arg	Leu	Lys	Glu	
		355					360					365				
Phe	Met	Glu	Tyr	Gln	Arg	Gln	Gly	Glu	Asp	Gln	Gly	Tyr	Trp	Lys	Val	
	370					375					380					
Arg	Gly	Leu	Asn	Asp	Val	Ile	Pro	Gly	Glu	Glu	Glu	Ile	Arg	Thr	Met	
385					390					395					400	
Ile	Thr	Pro	Glu	Asp	Ser	Ser	Leu	Met	Asp	Thr	Met	Gln	Phe	Gly	Gln	
				405					410					415		
Gln	Val	Leu	Asp	Asp	Asn	Met	Val	Leu	Phe	Gly	Glu	Gln				
			420					425								

<210> 8
 <211> 434
 <212> PRT
 <213> S. cerevisiae

<400> 8
 Met Thr Pro Asn Leu Lys Phe Ser Gly Gly Tyr Lys Leu Lys Ser Leu
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 Ile Glu Asp Val Ala Glu Asp Trp Gln Trp Asp Glu Asp Met Ile Ile
 20 25 30
 Asp Ala Lys Leu Lys Glu Ser Lys His Ala Glu Leu Asn Met Asn Asp
 35 40 45
 Glu Lys Leu Leu Leu Met Ile Glu Lys Thr Asn Asn Leu Ala Gln Gln
 50 55 60
 Lys Gln Gln Leu Asp Ser Ser Asn Leu Ile Leu Pro Leu Asn Glu Thr
 65 70 75 80
 Ile Leu Gln Gln Lys Phe Asn Leu Ser Asn Asp Asp Lys Tyr Gln Ile
 85 90 95
 Leu Lys Lys Thr His Gln Thr Lys Val Arg Ser Thr Ile Ser Asn Leu
 100 105 110
 Asn Ile Gln His Ser Gln Pro Ala Ile Asn Leu Gln Ser Pro Phe Tyr
 115 120 125
 Lys Val Ala Val Pro Arg Tyr Gln Leu Arg His Phe His Arg Glu Asn
 130 135 140
 Phe Gly Ser His Ile Arg Pro Gly Thr Lys Ile Val Phe Ser Lys Leu
 145 150 155 160
 Lys Ala Arg Lys Arg Lys Arg Asp Lys Gly Lys Asp Val Lys Glu Ser
 165 170 175
 Phe Ser Thr Ser Gln Asp Leu Thr Ile Gly Asp Thr Ala Pro Val Tyr
 180 185 190
 Leu Met Glu Tyr Ser Glu Gln Thr Pro Val Ala Leu Ser Lys Phe Gly
 195 200 205
 Met Ala Asn Lys Leu Ile Asn Tyr Tyr Arg Lys Ala Asn Glu Gln Asp
 210 215 220
 Thr Leu Arg Pro Lys Leu Pro Val Gly Glu Thr His Val Leu Gly Val
 225 230 235 240
 Gln Asp Lys Ser Pro Phe Trp Asn Phe Gly Phe Val Glu Pro Gly His
 245 250 255
 Ile Val Pro Thr Leu Tyr Asn Asn Met Ile Arg Ala Pro Val Phe Lys
 260 265 270
 His Asp Ile Ser Gly Thr Asp Phe Leu Leu Thr Lys Ser Ser Gly Phe
 275 280 285
 Gly Ile Ser Asn Arg Phe Tyr Leu Arg Asn Ile Asn His Leu Phe Thr
 290 295 300
 Val Gly Gln Thr Phe Pro Val Glu Glu Ile Pro Gly Pro Asn Ser Arg
 305 310 315 320
 Lys Val Thr Ser Met Lys Ala Thr Arg Leu Lys Met Ile Ile Tyr Arg
 325 330 335
 Ile Leu Asn His Asn His Ser Lys Ala Ile Ser Ile Asp Pro Ile Ala
 340 345 350
 Lys His Phe Pro Asp Gln Asp Tyr Gly Gln Asn Arg Gln Lys Val Lys
 355 360 365

Glu	Phe	Met	Lys	Tyr	Gln	Arg	Asp	Gly	Pro	Glu	Lys	Gly	Leu	Trp	Arg
	370					375					380				
Leu	Lys	Asp	Asp	Glu	Lys	Leu	Leu	Asp	Asn	Glu	Ala	Val	Lys	Ser	Leu
385					390					395					400
Ile	Thr	Pro	Glu	Gln	Ile	Ser	Gln	Val	Glu	Ser	Met	Ser	Gln	Gly	Leu
				405					410					415	
Gln	Phe	Gln	Glu	Asp	Asn	Glu	Ala	Tyr	Asn	Phe	Asp	Ser	Lys	Leu	Lys
			420					425					430		
Ser	Leu														

<210> 9
 <211> 415
 <212> PRT
 <213> S. pombe

<400> 9

Val	Asn	Lys	Thr	Asn	Gln	Ser	Ser	Phe	Phe	Ile	Asp	Lys	Ser	Leu	Val
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Asp	Ile	Asp	Phe	Ala	Phe	Asp	Glu	Asn	Ile	Phe	Asp	Gly	Asp	Thr	Gly
			20					25					30		
Thr	Ser	Lys	Val	Val	Leu	Asn	Leu	Asn	Asp	Pro	Lys	Leu	Leu	Leu	Gln
		35				40						45			
Pro	Gln	Leu	Pro	Lys	Lys	Glu	Asp	Ser	Gln	Arg	Ser	Phe	Ala	Asp	Thr
50					55						60				
His	Gln	Arg	Asn	Ser	Leu	Ala	Trp	Lys	Phe	Asn	Ile	Ser	Asn	Asp	Pro
65				70						75					80
Ala	Tyr	Glu	Met	Leu	Lys	Gln	Asn	His	Gln	Ser	Lys	Val	Arg	Asn	Thr
			85						90					95	
Leu	Ser	Gln	Leu	Ala	Ile	Glu	His	Ala	Ala	Phe	Ala	Glu	Lys	Leu	Thr
			100					105					110		
Phe	Pro	Tyr	Tyr	Lys	Thr	Arg	Leu	Ser	Lys	Arg	Ala	Val	Arg	Ser	Tyr
		115					120					125			
His	Arg	Pro	Thr	Met	Ser	Phe	Lys	Pro	Asn	Ala	Ala	Ile	Val	Phe	Ser
130					135						140				
Pro	Leu	Ile	Val	Arg	Lys	Arg	Ser	Lys	Asp	Lys	His	Lys	Ser	Glu	Arg
145					150					155					160
Glu	Leu	Ile	Pro	Thr	Thr	Lys	Glu	Ile	Thr	Met	Gly	Asp	Thr	Thr	His
				165					170					175	
Ala	Ile	Leu	Val	Glu	Phe	Ser	Glu	Glu	His	Pro	Ala	Val	Leu	Ser	Asn
			180					185					190		
Ala	Gly	Met	Ala	Ser	Arg	Ile	Val	Asn	Tyr	Tyr	Arg	Lys	Lys	Asn	Glu
		195					200					205			
Gln	Asp	Glu	Ser	Arg	Pro	Lys	Leu	Glu	Val	Gly	Glu	Ser	His	Val	Leu
210					215						220				
Asp	Val	Gln	Asp	Arg	Ser	Pro	Phe	Trp	Asn	Phe	Gly	Ser	Val	Glu	Pro
225					230					235					240
Gly	Glu	Ile	Thr	Pro	Thr	Leu	Tyr	Asn	Lys	Met	Ile	Arg	Ala	Pro	Leu
				245					250					255	
Phe	Lys	His	Glu	Val	Pro	Pro	Thr	Asp	Phe	Ile	Leu	Ile	Arg	Asn	Ser
			260					265					270		
Ser	Ser	Tyr	Gly	Ser	Lys	Tyr	Tyr	Leu	Lys	Asn	Ile	Asn	His	Met	Phe

		275					280				285					
Val	Ser	Gly	Gln	Thr	Phe	Pro	Val	Thr	Asp	Val	Pro	Gly	Pro	His	Ser	
	290					295					300					
Arg	Lys	Val	Thr	Thr	Ala	Ser	Lys	Asn	Arg	Leu	Lys	Met	Leu	Val	Phe	
305					310					315					320	
Arg	Leu	Ile	Arg	Arg	Ser	Pro	Asn	Gly	Gly	Leu	Phe	Ile	Arg	Gln	Leu	
				325					330					335		
Ser	Lys	His	Phe	Ser	Asp	Gln	Asn	Glu	Met	Gln	Ile	Arg	Gln	Arg	Leu	
			340					345					350			
Lys	Glu	Phe	Met	Glu	Tyr	Lys	Lys	Lys	Gly	Asp	Gly	Pro	Gly	Tyr	Trp	
		355					360					365				
Lys	Leu	Lys	Ser	Asn	Glu	Val	Val	Pro	Asp	Glu	Ala	Gly	Thr	Arg	Ser	
	370					375					380					
Met	Val	Ser	Pro	Glu	Thr	Val	Cys	Leu	Leu	Glu	Ser	Met	Gln	Val	Gly	
385					390					395					400	
Val	Arg	Gln	Leu	Glu	Asp	Ala	Gly	Tyr	Gly	Lys	Thr	Met	Asp	Glu		
				405					410					415		

<210> 10
 <211> 481
 <212> PRT
 <213> Homo sapiens

		<400>	10													
Ser	Leu	Ala	Gly	Trp	Leu	Pro	Ser	Ser	Met	Thr	Arg	Asn	Ala	Met	Ala	
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Tyr	Asn	Val	Gln	Gln	Gly	Phe	Ala	Ala	Thr	Leu	Asp	Asp	Asp	Lys	Pro	
			20					25					30			
Trp	Tyr	Ser	Ile	Phe	Pro	Ile	Asp	Asn	Glu	Asp	Leu	Val	Tyr	Gly	Arg	
		35					40					45				
Trp	Glu	Asp	Asn	Ile	Ile	Trp	Asp	Ala	Gln	Ala	Met	Pro	Arg	Leu	Leu	
	50					55					60					
Glu	Pro	Pro	Val	Leu	Thr	Leu	Asp	Pro	Asn	Asp	Glu	Asn	Leu	Ile	Leu	
65					70					75					80	
Glu	Ile	Pro	Asp	Glu	Lys	Glu	Glu	Ala	Thr	Ser	Asn	Ser	Pro	Ser	Lys	
			85						90					95		
Glu	Ser	Lys	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Ser	Arg	Ile	Leu	Leu	Gly	
			100					105					110			
Lys	Thr	Gly	Val	Ile	Lys	Glu	Glu	Pro	Gln	Gln	Asn	Met	Ser	Gln	Pro	
		115					120					125				
Glu	Val	Lys	Asp	Pro	Trp	Asn	Leu	Ser	Asn	Asp	Glu	Tyr	Tyr	Tyr	Pro	
	130					135					140					
Lys	Gln	Gln	Gly	Leu	Arg	Gly	Thr	Phe	Gly	Gly	Asn	Ile	Ile	Gln	His	
145					150					155					160	
Ser	Ile	Pro	Ala	Val	Glu	Leu	Arg	Gln	Pro	Phe	Phe	Pro	Thr	His	Met	
				165					170					175		
Gly	Pro	Ile	Lys	Leu	Arg	Gln	Phe	His	Arg	Pro	Pro	Leu	Lys	Lys	Tyr	
			180					185					190			
Ser	Phe	Gly	Ala	Leu	Ser	Gln	Pro	Gly	Pro	His	Ser	Val	Gln	Pro	Leu	
	195						200					205				
Leu	Lys	His	Ile	Lys	Lys	Lys	Ala	Lys	Met	Arg	Glu	Gln	Glu	Arg	Gln	
	210					215					220					

Ala	Ser	Gly	Gly	Gly	Glu	Met	Phe	Phe	Met	Arg	Thr	Pro	Gln	Asp	Leu
225					230					235					240
Thr	Gly	Lys	Asp	Gly	Asp	Leu	Ile	Leu	Ala	Glu	Tyr	Ser	Glu	Glu	Asn
				245					250					255	
Gly	Pro	Leu	Met	Met	Gln	Val	Gly	Met	Ala	Thr	Lys	Ile	Lys	Asn	Tyr
			260					265					270		
Tyr	Lys	Arg	Lys	Pro	Gly	Lys	Asp	Pro	Gly	Ala	Pro	Asp	Cys	Lys	Tyr
		275					280					285			
Gly	Glu	Thr	Val	Tyr	Cys	His	Thr	Ser	Pro	Phe	Leu	Gly	Ser	Leu	His
	290					295					300				
Pro	Gly	Gln	Leu	Leu	Gln	Ala	Phe	Glu	Asn	Asn	Leu	Phe	Arg	Ala	Pro
305					310				315						320
Ile	Tyr	Leu	His	Lys	Met	Pro	Glu	Thr	Asp	Phe	Leu	Ile	Ile	Arg	Thr
				325					330					335	
Arg	Gln	Gly	Tyr	Tyr	Ile	Arg	Glu	Leu	Val	Asp	Ile	Phe	Val	Val	Gly
			340					345					350		
Gln	Gln	Cys	Pro	Leu	Phe	Glu	Val	Pro	Gly	Pro	Asn	Ser	Lys	Arg	Ala
		355					360					365			
Asn	Thr	His	Ile	Arg	Asp	Phe	Leu	Gln	Val	Phe	Ile	Tyr	Arg	Leu	Phe
	370					375					380				
Trp	Lys	Ser	Lys	Asp	Arg	Pro	Arg	Arg	Ile	Arg	Met	Glu	Asp	Ile	Lys
385				390						395					400
Lys	Ala	Phe	Pro	Ser	His	Ser	Glu	Ser	Ser	Ile	Arg	Lys	Arg	Leu	Lys
				405					410					415	
Leu	Cys	Ala	Asp	Phe	Lys	Arg	Thr	Gly	Met	Asp	Ser	Asn	Trp	Trp	Val
			420					425					430		
Leu	Lys	Ser	Asp	Phe	Arg	Leu	Pro	Thr	Glu	Glu	Glu	Ile	Arg	Ala	Met
		435					440					445			
Val	Ser	Pro	Glu	Gln	Cys	Cys	Ala	Tyr	Tyr	Ser	Met	Ile	Ala	Ala	Glu
	450					455					460				
Gln	Arg	Leu	Lys	Asp	Ala	Gly	Tyr	Gly	Glu	Lys	Ser	Phe	Phe	Ala	Pro
465					470					475					480
Glu															

<210> 11
 <211> 74
 <212> PRT
 <213> C. albicans

<400> 11															
Asp	Ala	Glu	Asn	Gly	Asp	Asp	Ile	Asn	Lys	Asp	Lys	Glu	Lys	Glu	Val
1				5					10					15	
Glu	Lys	Glu	Lys	Glu	Gln	Glu	Arg	Glu	Glu	Glu	Lys	Gly	Lys	Asp	Lys
			20					25					30		
Glu	Lys	Asp	Lys	Asp	Lys	Glu	Lys	Asp	Lys	Thr	Glu	Lys	Glu	Lys	Ser
		35					40					45			
Lys	Lys	Ser	Lys	Glu	Gln	Asp	Thr	Glu	Ile	Asp	Val	Glu	Glu	Glu	Leu
	50					55					60				
Ala	Pro	Trp	Asn	Leu	Ser	Arg	Asn	Phe	Val						
65					70										

<210> 12
 <211> 18
 <212> DNA
 <213> "Artificial Sequence"
 <220>
 <223> sequence source: Degenerate oligonucleotide designed and used
 to amplify fragments of DNA from *Candida albicans* strain SC5314 genomic
 DNA by polymerase chain reaction. n is defined as Inosine.

<400> 12
 ccwggwccwa aytcnadd 18

<210> 13
 <211> 23
 <212> DNA
 <213> "Artificial Sequence"
 <220>
 <223> sequence source: Degenerate oligonucleotide designed and used
 to amplify fragments of DNA from *Candida albicans* strain SC5314 genomic
 DNA by polymerase chain reaction.

<400> 13
 gayccwachg gwtgtggwga agg 23

<210> 14
 <211> 24
 <212> DNA
 <213> "Artificial Sequence"
 <220>
 <223> sequence source: Degenerate oligonucleotide designed and used
 to amplify fragments of DNA from *Candida albicans* strain SC5314 genomic
 DNA by polymerase chain reaction.

<400> 14
 cctttcwcca cawccagtwg grtc 24

<210> 15
 <211> 19
 <212> DNA
 <213> "Artificial Sequence"
 <220>
 <223> sequence source: Degenerate oligonucleotide designed and
 used to amplify fragments of DNA from *Candida albicans* strain SC5314
 genomic DNA by polymerase chain reaction. n is defined as Inosine.

<400> 15
 ttrtthcayc tnartgwcc 19

<210> 16
 <211> 30
 <212> DNA
 <213> "Artificial Sequence"

<220>
 <223> S. cerevisiae

 <400> 16
 ccgctcgaga tgacacccaa cttaaagttc 30

 <210> 17
 <211> 29
 <212> DNA
 <213> "Artificial Sequence"
 <220>
 <223> S. cerevisiae

 <400> 17
 cgcggtacca gagatttttag cttagaatc 29

 <210> 18
 <211> 37
 <212> DNA
 <213> "Artificial Sequence"
 <220>
 <223> C. albicans
 <400> 18
 ggaattccat atgcttttgc tcaacaatcc cttggac 37

 <210> 19
 <211> 32
 <212> DNA
 <213> "Artificial Sequence"
 <220>
 <223> C. albicans
 <400> 19
 cgcggtatccc tgctctgctc accgaataac ac 32

 <210> 20
 <211> 37
 <212> DNA
 <213> "Artificial Sequence"
 <220>
 <223> Homo sapiens

 <400> 20
 ggaattccat atgagcctgg caggctggct tccttct 37

 <210> 21
 <211> 33
 <212> DNA
 <213> "Artificial Sequence"
 <220>
 <223> Homo sapiens
 <400> 21
 ccgctcgagt tctggagcaa aaaaggattt ctc 33

<210> 22
 <211> 0
 <212> DNA
 <213> Homo sapiens

<400> 22

Met	Gly	Pro	Gly	Cys	Asp	Leu	Leu	Leu	Arg	Thr	Ala	Ala	Thr	Ile	Thr
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Ala	Ala	Ala	Ile	Met	Ser	Asp	Thr	Asp	Ser	Asp	Glu	Asp	Ser	Ala	Gly
			20					25					30		
Gly	Gly	Pro	Phe	Ser	Leu	Ala	Gly	Phe	Leu	Phe	Gly	Asn	Ile	Asn	Gly
		35					40					45			
Ala	Gly	Gln	Leu	Glu	Gly	Glu	Ser	Val	Leu	Asp	Asp	Glu	Cys	Lys	Lys
	50					55					60				
His	Leu	Ala	Gly	Leu	Gly	Ala	Leu	Gly	Leu	Gly	Ser	Leu	Ile	Thr	Glu
65					70					75					80
Leu	Thr	Ala	Asn	Glu	Glu	Leu	Thr	Gly	Thr	Asp	Gly	Ala	Leu	Val	Asn
			85						90					95	
Asp	Glu	Gly	Trp	Val	Arg	Ser	Thr	Glu	Asp	Ala	Val	Asp	Tyr	Ser	Asp
			100					105					110		
Ile	Asn	Glu	Val	Ala	Glu	Asp	Glu	Ser	Arg	Arg	Tyr	Gln	Gln	Thr	Met
		115					120					125			
Gly	Ser	Leu	Gln	Pro	Leu	Cys	His	Ser	Asp	Tyr	Asp	Glu	Asp	Asp	Tyr
	130					135					140				
Asp	Ala	Asp	Cys	Glu	Asp	Ile	Asp	Cys	Lys	Leu	Met	Pro	Pro	Pro	Pro
145					150					155					160
Pro	Pro	Pro	Gly	Pro	Met	Lys	Lys	Asp	Lys	Asp	Gln	Asp	Ser	Ile	Thr
			165						170					175	
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		180						185					190		
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	210					215					220				
Ser	Val	Thr	Glu	Leu	Phe	Pro	Glu	Phe	Arg	Pro	Gly	Lys	Val	Leu	Arg
225					230					235					240
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			245						250					255	
Ser	Ala	Arg	Arg	Lys	Arg	Lys	Lys	Lys	His	Arg	Glu	Leu	Ile	Gln	Glu
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Glu	Gln	Ile	Gln	Glu	Val	Glu	Cys	Ser	Val	Glu	Ser	Glu	Val	Ser	Gln
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Lys	Ser	Leu	Trp	Asn	Tyr	Asp	Tyr	Ala	Pro	Pro	Pro	Pro	Pro	Glu	Gln
	290					295					300				
Cys	Leu	Ser	Asp	Asp	Glu	Ile	Thr	Met	Met	Ala	Pro	Val	Glu	Ser	Lys
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Phe	Ser	Gln	Ser	Thr	Gly	Asp	Ile	Asp	Lys	Val	Thr	Asp	Thr	Lys	Pro
			325						330					335	
Arg	Val	Ala	Glu	Trp	Arg	Tyr	Gly	Pro	Ala	Arg	Leu	Trp	Tyr	Asp	Met
			340					345					350		
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Phe	Arg	Lys	Leu	Glu	Glu	Asn	Asn	Gly	Thr	Asp	Leu	Leu	Ala	Asp	Glu
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Asn	Phe	Leu	Met	Val	Thr	Gln	Leu	His	Trp	Glu	Asp	Asp	Ile	Ile	Trp
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Asp	Gly	Glu	Asp	Val	Lys	His	Lys	Gly	Thr	Lys	Pro	Gln	Arg	Ala	Ser
			420					425					430		
Leu	Ala	Gly	Trp	Leu	Pro	Ser	Ser	Met	Thr	Arg	Asn	Ala	Met	Ala	Tyr
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	450					455					460				
Tyr	Ser	Ile	Phe	Pro	Ile	Asp	Asn	Glu	Asp	Leu	Val	Tyr	Gly	Arg	Trp
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Glu	Asp	Asn	Ile	Ile	Trp	Asp	Ala	Gln	Ala	Met	Pro	Arg	Leu	Leu	Glu
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Pro	Pro	Val	Leu	Thr	Leu	Asp	Pro	Asn	Asp	Glu	Asn	Leu	Ile	Leu	Glu
			500					505					510		
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		515					520					525			
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Val	Lys	Asp	Pro	Trp	Asn	Leu	Ser	Asn	Asp	Glu	Tyr	Tyr	Tyr	Pro	Lys
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			740					745					750		
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Lys Asp Glu Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His
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